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alpha-amylase having at least 70% homology to SEQ ID NO:13; wherein said three-dimensional alpha-amylase structure comprises calcium ions defined by atomic coordinates of Appendix 1;

(b) utilizing said three dimensional structure generated in step (a) and modeling methods to identify in said parent alpha-amylase structure at least one amino acid residue or structural part within 10Å of <sup>a calcium binding site</sup> calcium ions;

H2 I  
(c) modifying the sequence of a nucleic acid encoding said parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said at least one amino acid residue identified in step (b); and

(d) expressing the modified nucleic acid in a host cell to produce said variant alpha-amylase.

5 89. (amended) A method for producing a variant of a parent alpha-amylase having an altered property relative to said parent alpha-amylase, said method comprising

H3 I  
(a) generating a model of a three dimensional structure of a parent alpha-amylase, using a computer programmed for generating a model structure, said parent alpha-amylase having at least 70% homology to SEQ ID NO:13; wherein said three-dimensional alpha-amylase structure comprises an active site residue defined by atomic coordinates of Appendix 1;

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(b) utilizing said three dimensional structure generated in step (a) and modeling methods to identify in said parent alpha-amylase structure at least one amino acid residue or structural part within 15Å from <sup>an</sup> said active site residue;

(c) modifying the sequence of a nucleic acid encoding said parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said at least one amino acid residue identified in step (b); and

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(d) expressing the modified nucleic acid in a host cell to produce said variant alpha-amylase.

7 ~~91~~. (amended) A method for producing a variant of a parent alpha-amylase having an altered property relative to said parent alpha-amylase, said method comprising

*15*  
(a) generating a model of a three dimensional structure of a parent alpha-amylase, using a computer programmed for generating a model structure said parent alpha-amylase having at least 70% homology to SEQ ID NO:13; ~~wherein said three dimensional alpha amylase structure comprises a substrate binding site defined by atomic coordinates of Appendix 1;~~

*14*  
(b) utilizing said three dimensional structure generated in step (a) and modeling methods to identify in said parent alpha-amylase structure the substrate binding site;

*1*  
(c) modifying the sequence of a nucleic acid encoding said parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids <sup>*of the substrate binding site*</sup> ~~at a position corresponding to said at least one amino acid residue identified in step (b); and~~

*1*  
(d) expressing the modified nucleic acid in a host cell to produce said variant alpha amylase.